

RAW SEQUENCE LISTING

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Application Serial Number: 10/771,833
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PATENT APPLICATION: US/10/771,833

DATE: 10/29/2004

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Input Set : A:\39363106.app
 Output Set: N:\CRF4\10292004\J771833.raw

3 <110> APPLICANT: MILBURN, MICHAEL V.
 5 <120> TITLE OF INVENTION: PDE5A CRYSTAL STRUCTURE AND USES
 7 <130> FILE REFERENCE: 039363-1106
 9 <140> CURRENT APPLICATION NUMBER: 10/771,833
 10 <141> CURRENT FILING DATE: 2004-02-03
 12 <150> PRIOR APPLICATION NUMBER: 60/485,627
 13 <151> PRIOR FILING DATE: 2003-07-07
 15 <150> PRIOR APPLICATION NUMBER: 60/444,734
 16 <151> PRIOR FILING DATE: 2003-02-03
 18 <160> NUMBER OF SEQ ID NOS: 31
 20 <170> SOFTWARE: PatentIn Ver. 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 875
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
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 31 Pro Gln Gln Gln Lys Gln Gln Gln Arg Asp Gln Asp Ser Val Glu Ala
 32 20 25 30
 34 Trp Leu Asp Asp His Trp Asp Phe Thr Phe Ser Tyr Phe Val Arg Lys
 35 35 40 45
 37 Ala Thr Arg Glu Met Val Asn Ala Trp Phe Ala Glu Arg Val His Thr
 38 50 55 60
 40 Ile Pro Val Cys Lys Glu Gly Ile Arg Gly His Thr Glu Ser Cys Ser
 41 65 70 75 80
 43 Cys Pro Leu Gln Gln Ser Pro Arg Ala Asp Asn Ser Val Pro Gly Thr
 44 85 90 95
 46 Pro Thr Arg Lys Ile Ser Ala Ser Glu Phe Asp Arg Pro Leu Arg Pro
 47 100 105 110
 49 Ile Val Val Lys Asp Ser Glu Gly Thr Val Ser Phe Leu Ser Asp Ser
 50 115 120 125
 52 Glu Lys Lys Glu Gln Met Pro Leu Thr Pro Pro Arg Phe Asp His Asp
 53 130 135 140
 55 Glu Gly Asp Gln Cys Ser Arg Leu Leu Glu Leu Val Lys Asp Ile Ser
 56 145 150 155 160
 58 Ser His Leu Asp Val Thr Ala Leu Cys His Lys Ile Phe Leu His Ile
 59 165 170 175
 61 His Gly Leu Ile Ser Ala Asp Arg Tyr Ser Leu Phe Leu Val Cys Glu
 62 180 185 190
 64 Asp Ser Ser Asn Asp Lys Phe Leu Ile Ser Arg Leu Phe Asp Val Ala
 65 195 200 205
 67 Glu Gly Ser Thr Leu Glu Val Ser Asn Asn Cys Ile Arg Leu Glu

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68	210	215	220
70	Trp Asn Lys Gly Ile Val Gly His Val Ala Ala Leu Gly Glu Pro Leu		
71	225	230	235
73	Asn Ile Lys Asp Ala Tyr Glu Asp Pro Arg Phe Asn Ala Glu Val Asp		240
74	245	250	255
76	Gln Ile Thr Gly Tyr Lys Thr Gln Ser Ile Leu Cys Met Pro Ile Lys		
77	260	265	270
79	Asn His Arg Glu Glu Val Val Gly Val Ala Gln Ala Ile Asn Lys Lys		
80	275	280	285
82	Ser Gly Asn Gly Gly Thr Phe Thr Glu Lys Asp Glu Lys Asp Phe Ala		
83	290	295	300
85	Ala Tyr Leu Ala Phe Cys Gly Ile Val Leu His Asn Ala Gln Leu Tyr		
86	305	310	315
88	Glu Thr Ser Leu Leu Glu Asn Lys Arg Asn Gln Val Leu Leu Asp Leu		320
89	325	330	335
91	Ala Ser Leu Ile Phe Glu Glu Gln Gln Ser Leu Glu Val Ile Leu Lys		
92	340	345	350
94	Lys Ile Ala Ala Thr Ile Ile Ser Phe Met Gln Val Gln Lys Cys Thr		
95	355	360	365
97	Ile Phe Ile Val Asp Glu Asp Cys Ser Asp Ser Phe Ser Ser Val Phe		
98	370	375	380
100	His Met Glu Cys Glu Glu Leu Glu Lys Ser Ser Asp Thr Leu Thr Arg		
101	385	390	395
103	Glu His Asp Ala Asn Lys Ile Asn Tyr Met Tyr Ala Gln Tyr Val Lys		400
104	405	410	415
106	Asn Thr Met Glu Pro Leu Asn Ile Pro Asp Val Ser Lys Asp Lys Arg		
107	420	425	430
109	Phe Pro Trp Thr Thr Glu Asn Thr Gly Asn Val Asn Gln Gln Cys Ile		
110	435	440	445
112	Arg Ser Leu Leu Cys Thr Pro Ile Lys Asn Gly Lys Lys Asn Lys Val		
113	450	455	460
115	Ile Gly Val Cys Gln Leu Val Asn Lys Met Glu Glu Asn Thr Gly Lys		
116	465	470	475
118	Val Lys Pro Phe Asn Arg Asn Asp Glu Gln Phe Leu Glu Ala Phe Val		480
119	485	490	495
121	Ile Phe Cys Gly Leu Gly Ile Gln Asn Thr Gln Met Tyr Glu Ala Val		
122	500	505	510
124	Glu Arg Ala Met Ala Lys Gln Met Val Thr Leu Glu Val Leu Ser Tyr		
125	515	520	525
127	His Ala Ser Ala Ala Glu Glu Glu Thr Arg Glu Leu Gln Ser Leu Ala		
128	530	535	540
130	Ala Ala Val Val Pro Ser Ala Gln Thr Leu Lys Ile Thr Asp Phe Ser		
131	545	550	555
133	Phe Ser Asp Phe Glu Leu Ser Asp Leu Glu Thr Ala Leu Cys Thr Ile		560
134	565	570	575
136	Arg Met Phe Thr Asp Leu Asn Leu Val Gln Asn Phe Gln Met Lys His		
137	580	585	590
139	Glu Val Leu Cys Arg Trp Ile Leu Ser Val Lys Lys Asn Tyr Arg Lys		
140	595	600	605

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142 Asn Val Ala Tyr His Asn Trp Arg His Ala Phe Asn Thr Ala Gln Cys
143 610 615 620
145 Met Phe Ala Ala Leu Lys Ala Gly Lys Ile Gln Asn Lys Leu Thr Asp
146 625 630 635 640
148 Leu Glu Ile Leu Ala Leu Leu Ile Ala Ala Leu Ser His Asp Leu Asp
149 645 650 655
151 His Arg Gly Val Asn Asn Ser Tyr Ile Gln Arg Ser Glu His Pro Leu
152 660 665 670
154 Ala Gln Leu Tyr Cys His Ser Ile Met Glu His His His Phe Asp Gln
155 675 680 685
157 Cys Leu Met Ile Leu Asn Ser Pro Gly Asn Gln Ile Leu Ser Gly Leu
158 690 695 700
160 Ser Ile Glu Glu Tyr Lys Thr Thr Leu Lys Ile Ile Lys Gln Ala Ile
161 705 710 715 720
163 Leu Ala Thr Asp Leu Ala Leu Tyr Ile Lys Arg Arg Gly Glu Phe Phe
164 725 730 735
166 Glu Leu Ile Arg Lys Asn Gln Phe Asn Leu Glu Asp Pro His Gln Lys
167 740 745 750
169 Glu Leu Phe Leu Ala Met Leu Met Thr Ala Cys Asp Leu Ser Ala Ile
170 755 760 765
172 Thr Lys Pro Trp Pro Ile Gln Gln Arg Ile Ala Glu Leu Val Ala Thr
173 770 775 780
175 Glu Phe Phe Asp Gln Gly Asp Arg Glu Arg Lys Glu Leu Asn Ile Glu
176 785 790 795 800
178 Pro Thr Asp Leu Met Asn Arg Glu Lys Lys Asn Lys Ile Pro Ser Met
179 805 810 815
181 Gln Val Gly Phe Ile Asp Ala Ile Cys Leu Gln Leu Tyr Glu Ala Leu
182 820 825 830
184 Thr His Val Ser Glu Asp Cys Phe Pro Leu Leu Asp Gly Cys Arg Lys
185 835 840 845
187 Asn Arg Gln Lys Trp Gln Ala Leu Ala Glu Gln Gln Glu Lys Met Leu
188 850 855 860
190 Ile Asn Gly Glu Ser Gly Gln Ala Lys Arg Asn
191 865 870 875
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195 <211> LENGTH: 3106
196 <212> TYPE: DNA
197 <213> ORGANISM: Homo sapiens
199 <400> SEQUENCE: 2
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201 ggggtctcgag gccgagtcct gttcttctga gggacggacc ccagctgggg tggaaaagca 120
202 gtaccagaga gcctccgagg cgcgcgggtgc caaccatgga gcggggccggc cccagcttcg 180
203 ggcagcagcg acagcagcag cagccccagc agcagaagca gcagcagagg gatcaggact 240
204 cggtcgaagc atggctggac gatcactggg actttacctt ctcatacttt gttagaaaag 300
205 ccaccagaga aatggtcaat gcatggttt ctgagagagt tcacaccatc cctgtgtgca 360
206 aggaaggtat cagaggccac accgaatctt gctttgtcc cttgcagcag agtcctcg 420
207 cagataacag tgtccctgga acaccaacca gaaaaatctc tgcctctgaa tttgaccggc 480
208 ctcttagacc cattgttgc aaggattctg agggaaactgt gagttcctc tctgactcag 540
209 aaaagaagga acagatgcct ctaaccctc caaggttga tcatgatgaa gggaccagt 600

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210 gctcaagact cttggaatta gtgaaggata tttctagtca tttggatgtc acagccttat 660
 211 gtcacaaaat tttcttgcatt atccatggac tgatatctgc tgaccctat tccctgttcc 720
 212 ttgtctgtga agacagctcc aatgacaagt ttcttatcag ccgcctctt gatgttgctg 780
 213 aagggttcaac actggaagaa gtttcaaata actgtatccg cttagaatgg aacaaaggca 840
 214 ttgtgggaca tgtggcagcg cttggtgagc cttgaacat caaagatgca tatgaggatc 900
 215 ctcggttcaa tgcagaagtt gaccaaatta caggctacaa gacacaaaagc attctttgtta 960
 216 tgccaaattaa gaatcatagg gaagagggtt ttgggttagc ccaggccatc aacaagaaat 1020
 217 cagggaaacgg tgggacattt actgaaaaag atgaaaaggc ctttgctgct tatttggcat 1080
 218 tttgtggtat tggttctcat aatgctcagc tctatgagac ttcaactgctg gagaacaaga 1140
 219 gaaatcaggt gctgcttgac cttgcttagtt taattttgtta agaacaacaa tcattagaag 1200
 220 taatttgtaa gaaaatagct gcccacttata tctcttcat gcaagtgcag aaatgcacca 1260
 221 ttttcatagt ggtatgaaat tgctccgatt ctttttctag tgggttcac atggagtgtg 1320
 222 aggaattaga aaaatcatct gatacatcaa caagggaaaca tgatgcaaac aaaatcaatt 1380
 223 acatgtatgc tcagtagtgc aaaaatacta tggaaaccact taatatccca gatgtcagta 1440
 224 aggataaaaag atttccctgg acaactgaaa atacaggaaa tggtaaaccag cagtgcatta 1500
 225 gaagtttgct ttgtacacct ataaaaaaatg gaaagaagaa taaagtata ggggtttgcc 1560
 226 aacttgttaa taagatggag gagaatactg gcaaggttaa gccttcaac cggaaatgacg 1620
 227 aacagtttct ggaagctttt gtcattttt gtggcttggg gatccagaac acgcagatgt 1680
 228 atgaagcagt ggagagagcc atggccaagc aaatggtcac attggagggtt ctgtcgatc 1740
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 230 catctgccc gacccttaaa attactgact ttagcttcag tgactttgag ctgtctgatc 1860
 231 tggaaacagc actgtgtaca attcggatgt ttactgaccc caacccctgtg cagaacttcc 1920
 232 agatgaaaca tgaggttctt tgccatgttgc tttaagtgt taagaagaat tattcggaa 1980
 233 atgttgccta tcataattgg agacatgcct ttaatacagc tcagtgatc tttgctgctc 2040
 234 taaaagcagg caaaaattcag aacaagctga ctgacccctt gatacttgca ttgctgattt 2100
 235 ctgcactaag ccacgattt gatcacccgtg gtgtgaataa ctcttacata cagcgaagtg 2160
 236 aacatccact tgcccagctt tactgcccatt caatcatggc acaccatcat tttgaccagt 2220
 237 gcctgatgat tcttaatagt ccaggcaatc agattctcg tggcctctcc attgaagaat 2280
 238 ataagaccac gttgaaaata atcaagcaag ctatccatc tacagaccta gcaactgtaca 2340
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 241 caaaaaccctg gccttattcaa caacggatag cagaacttgt agcaactgaa ttttttgc 2520
 242 aaggagacag agagagaaaa gaactcaaca tagaaccac tggatctaattg aacagggaga 2580
 243 agaaaaacaa aatcccaagt atgcaagttt gggttcataga tgccatctgc ttgcaactgt 2640
 244 atgaggccctt gacccacgtg tcagaggact gtttccctt gctagatggc tgcaagaaaga 2700
 245 acaggccagaa atggcaggcc cttgcagaac agcaggagaa gatgtctgatt aatggggaaa 2760
 246 gcccggcaggc caagcggaaac tgagtggctt atttcattgc gagttgaagt ttacagagat 2820
 247 ggtgtgttctt gcaatatgcc tagtttctta cacactgtct gtatagtgtc tggatgttgc 2880
 248 atataacttttgc ccaactgtgtt atttttattt ttgcacaact tttgagagta tagcatgaat 2940
 249 gtttttagag gactattaca tattttttgtt atatttgc tatgtctactg aactgaaagg 3000
 250 atcaacaaca tccactgtta gcacattgtt aaaaaggattt tttgtgatat ttctgttactc 3060
 251 gcaaaatgttgc tgcaatgttgc ttgcactgag gttttttgtc ttgggg 3106
 254 <210> SEQ ID NO: 3
 255 <211> LENGTH: 33
 256 <212> TYPE: DNA
 257 <213> ORGANISM: Artificial Sequence
 259 <220> FEATURE:
 260 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 262 <400> SEQUENCE: 3

RAW SEQUENCE LISTING

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263 gtcgtatcat atgtcagcag cagaggaaga aac 33
 266 <210> SEQ ID NO: 4
 267 <211> LENGTH: 32
 268 <212> TYPE: DNA
 269 <213> ORGANISM: Artificial Sequence
 271 <220> FEATURE:
 272 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 274 <400> SEQUENCE: 4
 275 tctgcagtcg acaggccact cagttccgct tg 32
 278 <210> SEQ ID NO: 5
 279 <211> LENGTH: 391
 280 <212> TYPE: DNA
 281 <213> ORGANISM: Artificial Sequence
 283 <220> FEATURE:
 284 <223> OTHER INFORMATION: Description of Artificial Sequence: Pet15S construct
 286 <220> FEATURE:
 287 <221> NAME/KEY: CDS
 288 <222> LOCATION: (108)..(170)
 290 <400> SEQUENCE: 5
 291 agatctcgat ccccgaaat taatacgact cactataggg gaattgttag cgataacaa 60
 293 ttccccctcta gaaataattt tgtttaactt taagaaggag atatacc atg ggc agc 116
 294 Met Gly Ser
 295 1
 297 agc cat cat cat cat cac agc agc ggc ctg gtg ccg cgc ggc agc 164
 298 Ser His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
 299 5 10 15
 301 cat atg ggatccggaa ttcaaaggcc tacgtcgact agagcctgca gtctcgacca 220
 302 His Met
 303 20
 305 tcatcatcat catcattaat aaaagggcga attccagcac actggcgcc gttactatgt 280
 307 gatccggctg ctaacaaagc ccgaaaggaa gctgagttgg ctgctccac cgctgagcaa 340
 309 taactagcat aacccttgg ggcctctaaa cgggtcttga ggggtttttt g 391
 312 <210> SEQ ID NO: 6
 313 <211> LENGTH: 21
 314 <212> TYPE: PRT
 315 <213> ORGANISM: Artificial Sequence
 317 <220> FEATURE:
 318 <223> OTHER INFORMATION: Description of Artificial Sequence: Pet15S construct
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 321 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 322 1 5 10 15
 324 Arg Gly Ser His Met
 325 20
 329 <210> SEQ ID NO: 7
 330 <211> LENGTH: 6
 331 <212> TYPE: PRT
 332 <213> ORGANISM: Artificial Sequence
 334 <220> FEATURE:
 335 <223> OTHER INFORMATION: Description of Artificial Sequence: 6-His tag

VERIFICATION SUMMARY

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